

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2002, 02:17:48 ; Search time 733.22 Seconds
(without alignments)
1847.529 Million cell updates/sec

Title: US-09-719-748-1_COPY_98_886

Perfect score: 789
Sequence: 1 tatgacacgcgagagagct.....ctctcagacacccctgagtc 789

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_032802.*

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1: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT.*
2: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.*
3: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT.*
4: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT.*
5: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT.*
6: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT.*
7: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT.*
8: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT.*
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19: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT.*
20: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT.*
21: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.*
22: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	789	100.0	1742	21	AAZ49765	Human DAP-kinase-r
2	760.2	96.3	2353	21	AAZ73461	DNA encoding novel
3	495.2	62.8	2079	22	AAK94258	Human full-length
4	494.6	62.7	1429	20	AAK34657	Murine ZIP-kinase
5	493.6	62.6	2132	20	AAK34656	Human ZIP-kinase (
6	493.6	62.6	2224	22	AAH16158	Human cDNA sequenc
7	493.6	62.6	2224	22	AAH78068	Nucleotide sequenc
8	398.2	50.5	4272	16	AAO89839	Human death associ
9	398.2	50.5	5886	16	AAO89838	Human death associ

10	398.2	50.5	5886	19	AAV60289	DNA sequence encod
11	366.6	46.5	757	22	AAK91856	Human cDNA 5'-end
12	366.6	46.5	757	22	AAK93262	Human cDNA clone r
13	244.6	31.0	12638	22	AAK70641	Human Immune/haema
14	228.8	29.0	1120	22	ABAO9608	Human bone marrow
15	228.8	29.0	1505	22	ABAO9692	Human bone marrow
16	202.8	25.7	3192	21	AAFI6067	Human prostate can
17	193.6	24.5	480	21	AAZ29731	cDNA encoding huma
18	193.6	24.5	1864	21	AAZ29730	cDNA encoding huma
19	187.2	23.7	873	22	AAH46902	CDNA encoding huma
20	176.6	22.4	1776	22	AAH4679	Novel protein kina
21	173	21.9	539	22	AAH06178	Human cDNA clone (
22	166.8	21.1	3284	23	ABLI18303	Drosophila melanog
23	166.8	21.1	3374	23	ABLI1987	Drosophila melanog
24	166.2	21.1	2562	23	ABLI03417	Drosophila melanog
25	164.8	20.9	1836	22	AAK506721	Polynucleotide seq
26	164.8	20.9	2046	22	AAH78263	Nucleotide sequenc
27	163.8	20.8	2625	22	AAH44661	Novel protein kina
28	163.8	20.8	5532	20	AAZ25100	Human ischemic he
29	163.4	20.7	3864	22	AAH44664	Novel protein kina
30	163.4	20.7	5355	20	AAH89220	Seq ID No: 28 of W
31	163.4	20.7	5355	20	AAH89221	Seq ID No: 30 of W
32	163.4	20.7	5355	21	AAZ39404	Human Trad protein
33	163.4	20.7	5355	21	AAZ39405	Human Trad protein
34	163.2	20.7	1839	24	AAD26573	Human POLY4 cDNA.
35	162	20.5	2671	22	AAH44650	Novel protein kina
36	161.8	20.5	1971	24	AAD26571	Human POLY2 cDNA.
37	161.8	20.5	2558	24	AAD26572	Human POLY3 cDNA.
38	161.4	20.5	1917	23	ABLO3333	Drosophila melanog
39	154	19.5	513	22	ABA60848	Human foetal liver
40	154	19.5	513	22	ABA28854	Probe #7320 for ge
41	154	19.5	513	22	AAK09135	Human brain expres
42	154	19.5	513	22	AAK5024	Human bone marrow
43	154	19.5	513	22	AAH16902	Probe #835 for ge
44	154	19.5	513	22	AAH40741	Probe #9427 used t
45	153.6	19.5	2973	24	AAD26453	Human kinase PKIN-

ALIGNMENTS

RESULT 1	
AAZ49765	standard; DNA; 1742 BP.
AAZ49765	
AC	AAZ49765;
XX	
XX	
DT	18-Apr-2000 (first entry)
XX	
DE	Human DAP-kinase-related protein 1 (DRP-1) encoding DNA.
XX	
KW	DAP-kinase-related protein 1; DRP-1; Death-Associated Protein;
KW	calmodulin-dependent serine/threonine kinase; apoptosis; dimerisation;
KW	cytosolic; antiproliferative; immunosuppressive; metastasis; tumour; human;
KW	treatment; cancer; psoriasis; autoimmune disease; screening; ds.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	62..1144
FT	/tag= a
FT	/product= "DAP-kinase-related protein 1"
FT	1720..1725
FT	/tag= b
FT	
PN	W09966030-A1.
XX	
PD	23-DEC-1999.
XX	
XX	
PF	15-JUN-1999;
XX	
XX	99WO-US13411.
PR	
PR	15-JUN-1998;
XX	98US-0089294.
XX	

CC at fcp.wipo.int/pub/published_pct_sequences.
XX
Sequence 1253 BP; 331 A; 303 C; 366 G; 253 T; 0 other;

Query Match 96.3%; Score 760.2; DB 23; Length 1253;
Best Local Similarity 99.6%; Pred. No. 2.2e-207;
Matches 762; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 25 agtggccagtttcgcatcgtgaagaagtcgaggagaagacaggggttgatgca 84
    |||
DB 231 agtggccagtttcgcatcgtgaagaagtcgaggagaagacaggggttgatgca 290

QY 85 gccgaagtcatacaagaagcgagcgagcgagcgagcgagcgagcgagcgagcgag 144
    |||
DB 291 gccgaagtcatacaagaagcgagcgagcgagcgagcgagcgagcgagcgagcgag 350

QY 145 atcgaagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 204
    |||
DB 351 atcgaagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 410

QY 205 gaagtcatacaagaagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 264
    |||
DB 411 gaagtcatacaagaagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 470

QY 265 ctctcgattctcggccgaagaagtgatcagtgaggaagggccacagcttcatc 324
    |||
DB 471 ctctcgattctcggccgaagaagtgatcagtgaggaagggccacagcttcatc 530

QY 325 aagcagatctcgtgagtgaggaagtgatcagtgaggaagggccacagcttcatc 384
    |||
DB 531 aagcagatctcgtgagtgaggaagtgatcagtgaggaagggccacagcttcatc 590

QY 385 aagcagataaataatcgtgtgaggaagaataatcccatccacacatcaagctgatt 444
    |||
DB 591 aagcagataaataatcgtgtgaggaagaataatcccatccacacatcaagctgatt 650

QY 445 gaatttgctggtcgcaggaataagagtgagtgagtgagtgagtgagtgagtgagtgag 504
    |||
DB 651 gaatttgctggtcgcaggaataagagtgagtgagtgagtgagtgagtgagtgagtgag 710

QY 505 ccggaattctgtcgcaggaataatgtgaactacagcccttggtctcgagagcgatcag 564
    |||
DB 711 ccggaattctgtcgcaggaataatgtgaactacagcccttggtctcgagagcgatcag 770

QY 565 tggagcagtgagcgatcagcagcagcagcagcagcagcagcagcagcagcagcagcag 624
    |||
DB 771 tggagcagtgagcgatcagcagcagcagcagcagcagcagcagcagcagcagcagcag 830

QY 625 agcgaagcaggaagaacacgtgcagaaataatcagctcagtgagtgagtgagtgagtgag 684
    |||
DB 831 agcgaagcaggaagaacacgtgcagaaataatcagctcagtgagtgagtgagtgagtgag 890

QY 685 ttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 744
    |||
DB 891 ttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 950

QY 745 cgggaacggtctcacaatccaagaggtctcagacacccctgagtc 789
    |||
DB 951 cgggaacggtctcacaatccaagaggtctcagacacccctgagtc 995
```

RESULT 3
AAK94258
ID AAK94258 standard; cDNA; 2079 BP.

XX AAK94258;
XX
XX 06-NOV-2001 (first entry)
DE Human full-length cDNA, SEQ ID NO: 2874.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

```
XX OS Homo sapiens.  
XX PN EP1130094-A2.  
XX  
XX 05-SEP-2001.  
XX  
XX 07-JUL-2000; 2000EP-0114089.  
XX  
XX 08-JUL-1999; 99JP-0194486.  
XX 11-JAN-2000; 2000JP-0118774.  
XX 02-MAY-2000; 2000JP-0183765.  
XX  
XX (HELI-) HELIX RES INST.  
XX  
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,  
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI: 2001-524255/58.  
XX P-PSDB: AAM93338.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their  
XX use in genetic manipulation -  
XX  
XX PS Claim 8; SEQ ID NO 2874; 1380bp + sequence listing; English.  
XX  
XX CC The invention relates to primers for synthesizing full length cDNA  
XX clones. 830 cDNA molecules encoding a human protein have been  
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
XX molecules have been determined. Primers for synthesizing the full length  
XX cDNA are useful for clarifying the function of the protein encoded by  
XX the cDNA. The full length clones were obtained by construction of full  
XX length enriched cDNA libraries that were synthesised by the oligo-capping  
XX method. The primers enable the production of the full length cDNA easily  
XX without any special methods. The present sequence is a full length  
XX human cDNA of the invention.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in CD-ROM format directly from EPO.  
XX  
XX SQ Sequence 2079 BP; 396 A; 626 C; 733 G; 324 T; 0 other;

Query Match 62.8%; Score 495.2; DB 22; Length 2079;  
Best Local Similarity 76.8%; Pred. No. 2.2e-131;  
Matches 605; Conservative 0; Mismatches 183; Indels 0; Gaps 0;



```
QY 1 tatgacatcggagagagagctgggagtgagccagtttgccatcgtgaagaagtcgaggag 60
 |||
DB 106 tatgagatggggagggagctgggagtcggcagcgccagtttgcatcgtgcggaagtcgaggag 165

QY 61 aagagcagcggttgatgagtcagccaagtccatcaagaagcgcgagcgaggagc 120
 |||
DB 166 aagagcagcggttgatgagtcagccaagtccatcaagaagcgcgagcgaggagc 225

QY 121 cggcgagtgtagcgagcgaggaagatcgagggagtgaggaatccctcgagcgagtgctg 180
 |||
DB 226 cggcgagtgtagcgagcgaggaagatcgagggagtgaggaatccctcgagcgagtgctg 285

QY 181 caccacaatgtcatcagcgtgcagcagcgtctatagaaacgcgacagcagtgtagacatc 240
 |||
DB 286 caccacaatgtcatcagcgtgcagcagcgtctatagaaacgcgacagcagtgtagacatc 345

QY 241 ctgagctagtgcttgaggaagagctcttgatcttcctgcgcaggaagagagtgagtcagc 300
 |||
DB 346 ctgagctagtgcttgaggaagagctcttgatcttcctgcgcaggaagagagtgagtcagc 405

QY 301 gagagagagcgaccacgaactcatlaagcagatcctgtaggggtgaaactacatcacaca 360
 |||
DB 406 gagagagagcgaccacgaactctcaagcagatcctgtaggggtgaaactacatcacatc 465

QY 361 aagaataatgtcatttgatcctcaagccagaacaatlatgtgttagacaagaataatc 420
 |||
DB 466 aagcgatcagacaacttgatcctgaagcgcggaacaatcatcgtctgagacaagaacgtg 525
```


```

The invention provides human and murine recombinant zipper interacting protein kinase (ZIP-kinase) proteins. These proteins are serine/threonine kinases which bind the leucine zipper domain of transcription factor AP-4. Host cells containing vectors comprising the ZIP-kinase nucleic acids are used for the recombinant expression of the proteins. ZIP-kinase protein and DNA are useful as gene therapeutic agents against cancer, and as anti-cancer agents. The present sequence represents a DNA encoding a

01-JUL-1999 (first entry)

XX Human ZIP-kinase (serine/threonine kinase) encoding DNA.
 DE
 XX
 XX Zipper Interacting Protein Kinase; ZIP-kinase; serine/threonine kinase;
 KW leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
 KW Human; murine; ss.
 XX
 OS Homo sapiens.
 XX
 XX EP911408-A2.
 PN
 XX
 XX 28-APR-1999.
 PD
 XX
 XX 24-SEP-1998; 98EP-0307747.
 PF
 XX
 XX 26-SEP-1997; 97JP-0261589.
 PR
 XX
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX Akira S. Kawal T;
 PI
 XX
 XX WPI: 1999-246420/21.
 DR
 DR P-PSDB: AAY06921.
 XX
 PT New Recombinant Zipper Interacting Protein Kinase (ZIP-kinase)
 PT protein and DNA, useful as anticancer agents
 XX
 PS Claim 5; Page 15-18; 33pp; English.
 XX
 CC The invention provides human and murine recombinant zipper interacting
 CC protein kinase (ZIP-kinase) proteins. These proteins are serine/threonine
 CC kinases which bind the leucine zipper domain of transcription factor
 CC ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic
 CC acids are used for the recombinant expression of the proteins. ZIP-kinase
 CC protein and DNA are useful as gene therapeutic agents against cancer, and
 CC as anti-cancer agents. The present sequence represents a DNA encoding a
 CC human ZIP kinase protein.
 XX
 SO Sequence 2132 BP; 429 A; 630 C; 741 G; 332 T; 0 other;

Query Match 62.6%; Score 493.6; DB 20; Length 2132;
 Best Local Similarity 76.6%; Pred. No. 6.3e-131;
 Matches 604; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 1 tatgacatcggaagagagctgggagctggccagcttgccatcgtaagaagtcgggag 60
 ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 DB 130 tatgagatggggagagagctgggagctggccagcttgccatcgtaagaagtcgggag 189
 || ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 QY 61 aagagcagcgggcttgagatcgagccaagtcatcaagaagcgggcagagccggcgagc 120
 || ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 DB 190 aagggcagcgggcagaagagatcgagccaagtcatcaagaagcgggcagagccggcgagc 249
 || ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 QY 121 cggcgagctgtagcgggagagatcgagcgggaggtgagcattcctcgcgagctgctg 180
 ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 DB 250 cggcgaggtgtagcgggagagatcgagcgggaggtgagcattcctcgcgaggtatccgg 309
 ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 QY 181 caccacaatgcatcacgctgcagcagctcatatgagaaccgcagcagctggtgacatc 240
 ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 DB 310 caccacaatgcatcacgctgcagcagctcatatgagaaccgcagcagctggtgacatc 369
 ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 QY 241 ctggagctagtgctggagagagccttcgattccttcgaccgagagaggtacatgagc 300
 || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 DB 370 ctggagctagtgctggagagagccttcgattccttcgaccgagagaggtacatgagc 429
 ||||| || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 QY 301 gagagagagggcagcagctcatatgaagcagatcctgagtgaggctgaactcctcacaca 360
 ||||| ||||| ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 DB 430 gagagagagggcagcagctcatatgaagcagatcctgagtgaggctgaactcctcacaca 489
 ||||| ||||| ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 QY 361 aagaaatgctcacttgatctgaagccagaacaacatagtgtgtagaacgaatatc 420
 || || || ||||| || || ||||| || || ||||| || || ||||| || || ||||| ||
 DB 490 aagcagatcgacacattgacgtgaagccggaacaacatagtgtgtagaacgaagtgt 549

QY 421 cccattccacacataagctgattgacttgctgctcagcgaataagaatgagtt 480
 ||||| ||||| ||||| || ||||| || || ||||| || || ||||| || || ||||| ||
 DB 550 cccaaaccagaaatcaagctccatcgacttcgcatcgcgacaagatcgagcggggaaac 609
 ||||| ||||| ||||| || ||||| || || ||||| || || ||||| || || ||||| ||
 QY 481 gaatttaagaatatcttttggaacgcccgaatttgcttcacagaatctgtaactcagag 540
 || || ||||| || || || || || || || || || || || || || || || || || || || || ||
 DB 610 gaggtaagaacatcttcgcgcaccccgagcttgctggccccagagatgtgaaactagag 669
 || || ||||| || || || || || || || || || || || || || || || || || || || || ||
 QY 541 cccctggcttgtagagctgcagatgtgagcagatagggcgctcatcaactacatccttaagt 600
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 DB 670 ccgctgggcttgtagagcgagcagatgtgagcagctgctcatcaactacatccttcagg 729
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 QY 601 ggaagcattcccttcctcgaggagacagcaggaagcaggaacactggcgaatcatcatcag 660
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 DB 730 ggtgcatcccgcttcctggcgagaccaaagcagagagcgtcaccacacatcctagccgtg 789
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 QY 661 agtaagacttgtagagagatctcttcagcagatcagcagagctggccaaagacttat 720
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 DB 790 aactagacttcgagcgaggtacttcagcaacacccagcagctggcgcaagacttcat 849
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 QY 721 cggaaagctctgtttaagaagagaccgggaacggtcacaatccaagaggtctcagagcac 780
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 DB 850 cgccgctgctgctcaaaagatcccaagcggagatgaccattgcccagagcctggaacat 909
 || || || || || || || || || || || || || || || || || || || || || || || || || ||
 QY 781 ccctgagat 788
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 DB 910 tcttgagat 917

RESULT 6
 AAH16158
 ID AAH16158 standard; cDNA; 2224 BP.
 XX
 XX AAH16158;
 AC
 XX
 XX 26-JUN-2001 (First entry)
 DT
 XX
 DE Human cDNA sequence SRQ ID NO:14925.
 XX
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 KW Homo sapiens.
 XX
 XX EP1074617-A2.
 PN
 XX
 PD 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INSTR.
 XX
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR
 XX
 DR WPI: 2001-318749/34.
 PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 14925; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of

Query Match	62.6%	Score 493.6	DB 22	Length 2224
Best Local Similarity	76.6%	Pred. No. 6.4e-131		
Matches 604; Conservative	0	Mismatches 184	Indels 0	Gaps 0

QY	1	tatgacatcggagaggaacctcgggaggtgccaagtctgcacatcgtgaagaagtgcgggag	60
Db	251	tatcagatggggaggaagactctggccgcccgaagtcttgatcgtctcggaaagtgcggcag	310
QY	61	aagagcacggggcttgagatcgcacgaagatcattcaagaagaacggcgagac	120
Db	311	aagggcacgggcgaaggagtacgcacgaatcattcaagaagcgcgcgtctgcatacagc	370
QY	121	cggcgcggtctgagacgggagagatcgaacggggaggtgagatcctcgcgcaagtgcgt	180
Db	371	cggcgctgggttgagacgggagagatcgaacggggaggtgagatcctcgcgcaagtgcgt	430
QY	181	caccacaatgtcagacacgctgcacgaagctcattcaagaacccgacgaaggttgacac	240
Db	431	caccccaacatcaccacacccctgcagacatccttcgaagaacaagacgagctgctccac	490
QY	241	cttgagcctagctgtgagagagagccttcgatctctcgcgccgaagagatcattag	300
Db	491	cttgagcctagctgtctcgcggagagcctcttgaatctctcgcggagagagatctgtagc	550
QY	301	gaggagagagcgacacagcttcattcaagaagaagctcgtgtgggggtgaactactaca	360
Db	551	gaggagagagcgacaccccgatctcctcaagaagatcccgagcggtctcactacctgac	610
QY	361	aagaaatctcaacttgatctcaagccaaanaaacattagtgttgtagacaagaata	420
Db	611	aagcgcatcgacaccttgacctgaagcggaaacaatcatcgtcgtgacagaagcgt	670
QY	421	ccccttcacaacaacgaagcgtatgactgtgtctgctcaccgaatagaagatgatt	480
Db	671	cccacaaccaagaatcaagctctacgcacttcggcatcggcacaagaatctgagcgggac	730
QY	481	gaatttaagaatatcttcctggagacgcggaaattgtctgcacagaatctgtaactacag	540
Db	731	gaattcaagaatactcttcggcaccccgagtgttgccccagagatgtgaaactatgag	790
QY	541	cccctgggtctggaggtctgacatgtgagacatagcggtcatcaccatcctcttaagt	600
Db	791	cccctgggtctggaggtctgacatgtgagacatagcggtcatcaccatcctctctgagc	850
QY	601	ggagacaccccttcctcgggagacacgaagaagaanaacatgccaatatcatatcag	660
Db	851	gggagatcccggtcccggtcgagaccaaagcagagagcgtcaccaaatctcagccgt	910
QY	661	agttagacttgatgaagaaatctcgaagcatacgaacgagctcggccaagattatt	720
Db	911	aactacgacttcgagcgagggtactctacgaacaacccggcggtcggccaagattatt	970

QY	721	cgsaagcttccttggttaagaagagaccgcggaacagcgtcacatccaagagccttcacgaac	780
Db	971	cgccgcgccttcgcgtccaagaatcccaagcggagaattaccattgcccacagagccttgaacat	1030
QY	781	ccctcgat	788
Db	1031	tcctcgat	1038

RESULT	7
AAH78068	
ID	AAH78068 standard; DNA; 2224 BP.

DT 26-NOV-2001 (first entry)

DE Nucleotide sequence of a human protein kinase/protein phosphatase.

KW Human; protein kinase; protein phosphatase; signal transduction,
intracellular signalling pathway; ss.

OS Homo sapiens.

Key	Location/Qualifiers
FH	
FT	
CDS	215..1579

FT /product="protein kinase/protein phosphatase"

PN WO200109345-A1

PD 08-FEB-2001

PF 28-JUL-2000; 2000WO-JP05060

PR 29-JUL-1999; 99JP-0248036

PR 11-JAN-2000; 2000JP-0118776

PR 02-MAY-2000; 2000JP-0183767

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Salto K, Yamamoto J;

PI Senoo C, Nezu J;
vv

DR WPI; 2001-564736/63

	Nov	2	6	9	7	5	8	3
XX								
DE								

Identifying modulators which can be used to treat human or animal disorders associated with the overexpression of mutant β -catenin

XX
 Claim 1: Dacc 110-125. 336000. Tcccccccc
 PS

The present sequence encodes a human protein kinase/protein phosphatase. The polypeptides are expected to participate in signal transduction in cells. The kinase phosphatases are connected with intracellular signalling pathways. Antisense oligonucleotides and compounds identified by screening (agonists or antagonists) can be used to treat human or animal disorders associated with the expression or function of the protein. In addition, the polypeptides may be used as target molecules for drug development.

SQ Sequence 2224 BP; 419 A; 656 C; 806 G; 343 T; 0 other;

Query Match	62.68;	Score 493.6;	DB 22;	Length 2224;
Best Local Similarity	76.68;	Pred. No. 6, 4e-131;		
Matches 604;	Conservative 0;	Mismatches 184;	Indels 0;	Gaps 0;

```

Oy 1 tatgacatcgagagagagctggagagtgccagatttgcacatcgttgaagaagtccggag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 tatgagatggggagagagctgggagagcgccagatttgcacatcgttgcggaagtccggag 310
Oy 61 aagagcaggggcttgagatctgacagcaagttcacaagaagcggcagagccgggagc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 aagggcagggcagagagatcgacagcaagttcacaagaagcggcgtcttgcacg 370
Oy 121 cggcgagctgtgagcgggagagatcgagcgggaggttgagcattctgcggcaggtctg 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 371 cggcgctggggtagcgggagagatcgagcgggaggttgagcattctgcggagtcgg 430
Oy 181 caccacaatgtcatcagcagcagcagcagctctatgagaacccgagcgtgtgtcattc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 431 caccacaatcatcaccctcgacagacattctcgagaacaagaagcagcgtgtcttcattc 490
Oy 241 ctgtgagctagtgctgagagagagattctcgattcttcggcccaagaagagtcattgatt 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 491 ctgtgagctgtctctgagcgggagctcttgcattctctgcgggagaggtctgctgagc 550
Oy 301 gaggagagagcagcagcattcatagaagatcctgtgagtggtgtaactattcacaaca 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 551 gaggagcagggcaccgctctctcacaagatccttgagcggcgttccattcattcattct 610
Oy 361 aagaaatctgtcattctgattctcacaagccagaacaattatgtgttagacaagaattatt 420
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Db 611 aagagcattcgacacatttgcattgaagccggaanaacattatgctgtggaagaagcgtg 670
Oy 421 cccattcacaacataagcgtgattgatttgcgtctgcagcaataagaagagagatt 480
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Db 671 cccaaaccagaatcagaatcattcattcgtcgtcgcagcaagatcggagcgggagac 730
Oy 481 gaatttaagaataatttttgagagcgggaatttgcctccagaatttgtaactaagag 540
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Db 731 gaggtaagaacattcttcgaccccgaggttctgtgcccagagatttgtaactatgag 790
Oy 541 ccccttggtctgtgagcgtgacatgtgagcagtagcgctacacattcattcatttaagt 600
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Db 791 ccggtggtcgtgagcgagacatgtgagcagtcgtgtcattcattcattcattcattc 850
Oy 601 ggaagatcccttctctggagagacagaaagaaacattcgtgcaaatatcatcagtg 660
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Db 851 ggttcattcccgcttccgtcgagcagaaagagagcgtccacaacattcagccgtg 910
Oy 661 agttacgacttgttgaggaatttctcagcatcagcagcggtcgccaaagatttatt 720
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Db 911 aactacgacttcgacggaggtactcagcaacacccgagcgtgccaaggttcat 970
Oy 721 cggagagcttctgttaagagagccggaaacggtcacaatccaaagaggtctcagacac 780
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Db 971 cggcggtgtgtctgtaaaagatcccaagcggagaaatgacattgcacagagccttgaacat 1030
Oy 781 cccctgag 788
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Db 1031 tccctgag 1038

```

RESULT 8

AA089839 ID AA089839 standard; cDNA; 4272 BP.

XX AC AA089839;

DT 04-JAN-1980 (first entry)

DE Human death associated protein DAP-2.

KW Death associated protein; DAP; cytokine; cell death; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..4272

```

FT XX /*tag= a
PN XX W09510630-A.
PD XX 20-APR-1995.
PE XX 12-OCT-1994; 94WO-US11598.
PR XX 12-OCT-1993; 93IL-0107250.
PA XX (RYCU/) RYCUS A.
XX XX (YEDA ) YEDA RES & DEV CO LTD.
PI XX Kimchi A;
XX WPI; 1995-1/8528/23.
DR DR P-PSDB; AAR74205.
PT PT DNA whose expression mediates cytokine-induced programmed cell
PT death - used to treat diseases or disorders associated with
PT uncontrolled, pathological cell growth or cytokine-induced
PT programmed cell death.
PS PS Claim 2; Fig 8; 61pp; English.
XX CC DAP genes seem to play an imp. role in programmed cell death and the
CC inhibition of their expression protects the cell from cytokine
CC promoted cell death. A cDNA library was generated from a mixture of
CC mRNAs harvested after treatment of HeLa cells with IFN-gamma. It
CC was cloned in antisense orientation into the EBV-based pTK01
CC expression vector. The resulting expression library was introduced
CC into HeLa cells. A fraction of the transfectants was selected with
CC hygromycin B. The majority of transfected cells were selected with
CC both hygromycin B and IFN-gamma. The cells that survived and/or
CC grew in the presence of IFN-gamma were expanded and pooled. The
CC extrachromosomal DNA was obtained and cleaved with DpnI and introduced
CC into E. coli HB101 host cells. A few bacterial clones were obtained
CC which included DNA antisense sequences, some of which were able to
CC protect cells from the death-promoting effects of IFN-gamma.
CC Plasmid DNAs were prepared from 10 individual bacterial clones. PCR
CC amplified cDNA inserts were generated from each plasmid using
CC primers that correspond to the immediate flanking sequence of the
CC cDNA insertion sites in the pTK01 vector. The PCR fragments were
CC used as labeled probes to search Southern blots for possible cross
CC hybridisation between some of the rescued antisense cDNA clones.
CC The 10 cDNA clones were classified into six distinct
CC non-overlapping groups, some constituting several members (clones)
CC and some constituting a single member. Antisense cDNA clone 256 has
CC the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and
CC used to screen a K562 lambda gt10 cDNA library. The resulting
CC composite sequence derived from 2 clones and the deduced AA sequence
CC are shown in AA089838 and AAR74205. The ORF is also shown in AA089839.
CC AA089838 has a poly A tail. The calculated mol. wt. of the protein
CC is about 160 kDa. Several known domains and motifs were identified
CC in the protein (see AA074205 FT).
XX XX
SQ Sequence 4272 BP; 1076 A; 1161 C; 1121 G; 914 T; 0 other;

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Query Match 50.5%; Score 398.2; DB 16; Length 4272;

Best Local Similarity 70.6%; Pred. No. 1.8e-103; Matches 557; Conservative 0; Mismatches 208; Indels 24; Gaps 1;

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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97 aaaaagtaacggcctccagatcccgcaaatcacaagaagagactaaatccagc 156
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 121 cggcggtgtgagccgggagagatcagcgggaggtgagcattcctgcggcaggtctg 180
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Db 157 cggcgggtgtgagcgcgagagacatcgagcggaggttcagcatccctgaaggatccac 216
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Db 217 caccacaatgtatcacatccctgcagcaggtctatggaacaaagcagcgtcatccgtacc 276
Oy 241 ctgtagtagtgtctggaagagctctgcattctcctgcccagaagagtcactgaat 300
Db 277 ttggaactcgtgtgaggtgagcagctgtgtgactctcttgatgcgaagaagaaatcttaact 336
Oy 301 gagggagggggccacacgactctatgaagacagatccctgagtggtgtgaactcctacaca 360
Db 337 gaagaggaagcaacccaatctctcaacaacatcttaagtgtgtactacactgcctc 396
Oy 361 aagaatgtcctactctgacatcgaacccaagaacatgatgtgttagaagaatatt 420
Db 397 ctccaatccgcacacttgcattgaagcctgagacaataagctcttgatagaatgtgc 456
Oy 421 cccattcacacatacaagctgattgacttggctgtcgcacgaatagaaatgagat 480
Db 457 cccaactcgtgacatgaatgactt-----tggaat 492
Oy 461 gaattagaatatttttggagcgcgggaattgtgtctcagaatgtgtgaactacagag 540
Db 493 gaattaaaaacataattggagctccagagttgtcgcctcctgagatagtcacatgaa 552
Oy 541 cccctgtgtctgagcgtgacatgtgagcagatagcgtcatcactacatcccttaagt 600
Db 553 cctctgtgtctgagcagatattgtgagatcgggtatcggtatataatatacctcctaagt 612
Oy 601 ggagcatccctctctcgtggagacacgagacgaagaacatggtgcaaatatcacatcagt 660
Db 613 ggggctcccatctctcgtgagacactaagcaagaacgltagcaaatgtatccgctgctc 672
Oy 661 agttacgacttgatgaggaatcttcagccatagcagcgtgccaagacttatt 720
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Db 723 agaagactctcgtgtcgaagatcccaagaagaagaaatgacaaatcgaatgtgtcagact 792
Oy 781 cccctgagatc 789
Db 793 cccctgagatc 801

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RESULT 9

AA089838
ID AA089838 standard; cDNA; 5886 BP.

XX AC AA089838;

XX 04-JAN-1980 (first entry)

XX DE Human death associated protein DAP-2.

XX KW Death associated protein; DAP; cytokine; cell death; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 337..4605

XX FT /tag= a /note= "claimed"

XX FT /tag= b /tag= c

XX FT /tag= d /tag= e

XX FT misc_feature 5103..5107

XX FT misc_feature 5103..5107

```

FT FT /tag= e
FT FT /label= instability motif
PN PN
XX MO9510630-A.
XX PD 20-APR-1995.
XX PF 12-OCT-1994; 94MO-US11598.
XX PR 12-OCT-1993; 93IL-0107250.
XX PA (RYCUS/) RYCUS A.
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PI Kimchi A;
XX DR WPI. 1995-178528/23.
XX P-PSDB; AAR74205.
XX PT DNA whose expression mediates cytokine-induced programmed cell
XX PT death - used to treat diseases or disorders associated with
XX PT uncontrolled, pathological cell growth or cytokine-induced
XX PS Claim 2; Fig 8; 61pp; English.
XX
XX DAP genes seem to play an imp. role in programmed cell death and the
XX inhibition of their expression protects the cell from cytokine-
XX promoted cell death. A cDNA library was generated from a mixture of
XX mRNAs harvested after treatment of HeLa cells with IFN-gamma. It
XX was cloned in antisense orientation into the EBV-based pTK01
XX expression vector. The resulting expression library was introduced
XX into HeLa cells. A fraction of the transfectants was selected with
XX hygromycin B. The majority of transfected cells were selected with
XX both hygromycin B and IFN-gamma. The cells that survived and/or
XX grew in the presence of IFN-gamma were expanded and pooled. The
XX extrachromosomal DNA was obtd. and cleaved with DpnI and introduced
XX into E. coli HB101 host cells. A few bacterial clones were obtd.
XX which included DNA antisense sequences, some of which were able to
XX protect cells from the death-promoting effects of IFN-gamma.
XX Plasmid DNAs were prepd. from 10 individual bacterial clones. PCR
XX amplified cDNA inserts were generated from each plasmid using
XX primers that corresp. to the immediate flanking sequence of the
XX cDNA insertion sites in the pTK01 vector. The PCR fragments were
XX used as labeled probes to search Southern blots for possible cross
XX hybridisation between some of the rescued antisense cDNA clones.
XX The 10 cDNA clones were classified into six distinct
XX non-overlapping gps., some constituting several members (clones)
XX and some constituting a single member. Antisense cDNA clone 256 has
XX the DNA product called DAP-2. Clone 256 (DAP-2) was sequenced and
XX used to screen a K562 lambda gt10 cDNA library. The resulting
XX composite sequence derived from 2 clones and the deduced AA sequence
XX are shown in AA089838 and AAR74205. The ORF is also shown in AA089839.
XX AA089838 has a poly A tail. The calculated mol. wt. of the protein
XX is about 160 kDa. Several known domains and motifs were identified
XX in the protein (see AA074205 FT).
XX
XX Sequence 5886 BP; 1447 A; 1524 C; 1500 G; 1415 T; 0 other:
XX
XX Query Match 50.5%; Score 398.2; DB 16; Length 5886;
XX Best Local Similarity 70.6%; Pred. No. 2,1e-103;
XX Matches 557; Conservative 0; Mismatches 208; Indels 24; Gaps 1;
Oy 1 tatgacatcgagagagctggtgggtgctgcatcgatgtgaagaagtcggggag 60
Db 373 taagacacgcggaggaacttggcagctgtgacagcttgcgtgtgaagaagtcgg 432
Oy 61 aagaagcaggggctgagatgcagcaagctcatcaaaagcggcagagccggggagc 120
Db 433 aaagtaaccggtctcagtatccgcgaatcatcaaaagagagagcgaatgcagc 492
Oy 121 cggcgggtgtgagcgcgagagacatcgagcggaggtgagacatccctgcagtgctg 180

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D	493	cgcgcggggctgtcgtgagccgcgagagacacacgagcgggaggtcagacatccctgaagagatccag	552
Q	181	caccacaatgtctcatctcagctctgcacgacgtcctcctgaagaacgcgacgagctgtgtacatc	240
D	553	caccaccaatgtctcatcaccctgcacgcgaggtctctatgagaaagaacgagcgtcatcctgttc	612
Q	241	ctctgagctagtgtctctgagagagagctctctcgattcttcctctcgcgcgaagagagctactagt	300
D	613	ctggaaactctgttcagaggttgcgcgactgttgcattctcttagcctcgaaagaaatcttaact	672
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Q	361	aagagaaattctcactattgtacatctcaagccgaagaacaaatattgtctgaacagaataat	420
D	733	ctctcaaatctgcaccacttgcattgtctcttaagccttgagaaacataatgtcttcttgatagaatgtc	792
Q	421	cccaatccacacatacaagctgattgtactctgtctgtctgcctcacgaataagaaatgagatgagat	480
D	793	cccaaacctctgcgtacaaagatcattgtact-----tgaaat	828
Q	481	gaatttaagataatttttggagacgcggaaattgttgcctccagaattgtgtgaactacagag	540
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Q	541	ccccctggctctgagagctctgacatgtgagacataagcgtcatcacctacatcccttaagt	600
D	889	ccctcttgctctcttgagacagataatgtgtggtatcgggtatataactatataccctcctaagt	948
Q	601	ggaagcaccctctctctctgaggagacagaaagcagaaacacctgcacaataatcatcacaatg	660
D	949	ggggccctcccatctctcttgagacacttaagcaagaagcttagcaaatgtatccgtctgc	1008
Q	661	agttacgactcttatgtagaatctctcagccacatacagcgcgagctgtgccaagacttatt	720
D	1009	aactacgaattcttgagatgtgaattcttcaatataccagctgccttagcacaagatttcata	1068
Q	721	cggaagctctgtcttaagaagagaccgcgaaacggtccacacatccagaaggtctctcagacac	780
D	1069	agaaagactcttcgggtcacaagagatcccaagaagagaaatgacaaatccaagatagtctgcagcat	1128
Q	781	ccctctgatac	789
D	1129	ccctctgatac	1137
RESULT 10			
AAV60289			
AAV60289 standard; DNA; 5886 BP.			
XX			
AAV60289;			
12-JAN-1999 (first entry)			
XX			
DNA sequence encoding death associated protein-2 (DAP-1, DAP-kinase).			
XX			
Death associated protein: DAP-2; cell death; tumour cell; DAP-kinase;			
KW metastatic activity; cancer; psoriasis; autoimmune disease;			
KW programmed cell death; degenerative neurological disease;			
KW Alzheimer's; ss.			
XX			
Homo sapiens.			
OS			
XX			
Key			
FH Location/Qualifiers			
CDS 337..4608			
FT /*tag= a			
FT /product= DAP-2			
XX			
W09839429-A2.			
XX			
11-SEP-1998.			
XX			

PF	03-MAR-1998;	98WO-IL00102.
XX		
PR	03-MAR-1997;	97US-0810712.
XX		
PA	(YEDA) YEDA RES & DEV CO LTD.	
XX		
PI	Kimchi A:	
XX		
DR	WPI: 1998-520781/44.	
XX	P-PSDB; AAM71367.	
PT	New isolated death associated protein nucleic acids - used for the	
PT	diagnosis and treatment or disorders associated with programmed cell	
XX	death, e.g. cancers, auto-immune disease or neurological disease	
PS	Claim 2; Fig 8; 157pp; English.	
XX		
CC	The present sequence encodes a death associated protein-2 (DAP-2,	
CC	DAP-kinase). The DAP genes and proteins are used for promoting death of	
CC	normal or tumour cells, and for suppressing the metastatic activity of	
CC	tumour cells. They can be used in the treatment of diseases or disorders	
CC	associated with uncontrolled pathological growth, e.g. cancer,	
CC	poriasis, autoimmune diseases and others. Agents which antagonise,	
CC	inhibit or neutralize DAP products are used for protecting cells from	
CC	programmed cell death. In this case they can be used for the treatment	
CC	of degenerative neurological diseases, e.g. Alzheimer's, prevention of	
CC	death of T cells in AIDS patients, prevention of rejection associated	
CC	cell death in transplants, and protection of normal cells from	
CC	the cytotoxic effects of anti-cancer therapies.	
XX		
SQ	Sequence 5886 BP; 1447 A; 1525 C; 1499 G; 1415 T; 0 other;	
	Query Match	50.5%; Score 398.2; DB 19; Length 5886;
	Best Local Similarity	70.6%; Pred. No. 2.1e-103;
	Matches 557; Conservative 0; Mismatches 208; Indels 24; Gaps	
OY	1 tatgacatcgagagagagactggggagatggccagtttgccatcgtgaagaagtgccggag	60
DB	373 taagcagccggcgagaaacttggcgttgacacglttgcggttgtaagaatagccgttga	432
OY	61 aagagcacggggcttgaatatacgaccaaagtcatacaagaagcggcgagccggcgagc	120
DB	433 aaagtacgcgcctccagatccgcgaattcatcaagaagaagagagactaagtcacgc	492
OY	121 cggcgcggtgtgagccggagagatcgagcgggaggttgagacatcttcgcggaggtgctg	180
DB	493 cggcggggtgttgagccggagacatcgagcgggaggttaagatctctgaagagatccag	552
OY	181 caccacaatgtatagaacttcgacagcgtctatggaaaccgacgcagcttgtagacatc	240
DB	553 caccacaatgtatataccctcgacagagtgctatgagaaagaagacgcatcctgac	612
OY	241 ctggagctagtgctcgagagagagctcttcgaattcttcggtcccgagagagtgactaggt	300
DB	613 ttggagccgttgagcggagtggtgctgttggacttcttagcgaagaagaatcttaact	672
OY	301 gaggagagagccacagctcataaagacagatcctgtagtgggtgaactactcttacaca	360
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OY	361 aagaaatgtgcactttgacttcaagccagagaacaatattatgtttgtagaagaatatt	420
DB	733 ctcaaatcgcaccacttgatccttaagcccgagacataatgcttcttgtagaagtgct	792
OY	421 ccacatccacacataaagctgattgacttggcttgctgcacgaataagatagatgagtt	480
DB	793 cccaactcgtgatcaagatcatgactt-----tggaaat	828
OY	481 gaatttaagaatatttttgggagccgggaatttgtctccagaatattgtgactaagag	540
DB	829 gaatttaagaacatltttggagctccagaagtttgcgtccctcgagatagtcacactatga	888

Sequence 757 BP: 176 A: 210 C: 220 G: 133 T: 11

08-JUL-1999; 99JP-0194486.
11-JAN-2000; 2000JP-0118774.

XX (HELI-) HELIX RES INST.
PA
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI: 2001-524255/58.
DR
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
PS
PS Example 11: SEQ ID NO 1722; 1380bp + sequence listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence was used in
CC representative sequence from a human clone which was used in
CC homology searches to identify the clone.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
XX Sequence 757 BP; 176 A; 219 C; 220 G; 133 T; 9 other;
SQ
Query Match 46.5%; Score 366.6; DB 22; Length 757;
Best Local Similarity 75.9%; Pred. No. 8.7e-95;
Matches 486; Conservative 0; Mismatches 151; Indels 3; Gaps 3;
QY 1 tatgacatcggagagagctgggagctggccagtttgcacatcgtgaagaagtcgaggag 60
DB 106 tatgacatcgggagagctgggagctggccagtttgcacatcgtgaggaagtcgaggag 165
QY 61 aagagcaacggggtctgagtatgcaacgaatcattcaagaagaacggcgagcgagc 120
DB 166 aaggacacgggagaaagatcagcagcaatcattcaagaagaacggcgagcgagc 225
QY 121 cggagcgtgtgagcgggagagatcagcgggaggtgagatcctcggcaggtgctg 180
DB 226 cggcgtgtggtgagcgggagagatcagcgggaggtgagatcctcggcaggtgctg 285
QY 181 caccacaatgtcatcagcgtgacagctctatgagaacccgacacgagctgtgacatc 240
DB 286 caccacaatcattcacccttgcagcatcttctgagaacaagaagagctgtcctc 345
QY 241 ctgtgacatgctgtcggaggaagctcttcgattcctcggcccaagaagagtcactgagt 300
DB 346 ctgagagctgtctcggcgggagctcttctgacctcctcggagaagaagagtcgctgagc 405
QY 301 gagagggagggcaccacgacttcaatgaagatcctggaatctgggtgagtcacacttcacaca 360
DB 406 gagagcgaagcaccacgaattcctcaagcagatcctggaagcgttcactactgcaactc 465
QY 361 aagaaatgtcacttgcattgcacgaacgaacaaatattgtgtttagacaagaata 420
DB 466 aagcagcatcgacacatttgacctggaacggaacaaacatcatctgtcgtgaagaagc 525
QY 421 cccattcacaataaagtgtgacttgtctggtcgtcgaagaatagaatgagatg 480
DB 526 cccaaccacgaatcaatcattcagctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 585
QY 481 gaatttaagaatatcttggagagcgcggaa-cttgttgcgtcgaagaatgttaacagca 539
DB 586 gaattcaanaaatacttgcgcaccccggaatttggcgcacaaatgttaactatga 645
QY 540 gccctgggtc-tggagagctgacatgtgagacatagcgctacacactacactcttaa 598
DB 646 accgctgggctctggaagcngacatgttgaacatcgtgtctccctatatcctcctgaa 705

QY 599 gtgagacat-cccccttctcgtggagacatcgaagcagga 637
DB 706 ccggtgcatccccccttctcgtggacaaacacacnaggana 745
RESULT 13
AAK70641
ID AAK70641 standard; DNA; 12638 BP.
XX
XX AAK70641;
AC
XX
XX 06-NOV-2001 (first entry)
DE Human Immune/Haematopoietic antigen genomic sequence SEQ ID NO:25453.
XX
XX Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
XX WO200157182-A2.
PD
XX
XX 09-AUG-2001.
PE 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226861.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0228287.
PR 01-SEP-2000; 2000US-0228343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.

Db 6336 cctcttgactctcgtgcggaagagctgcctgacgagagcgagccaccagttcttc 6395
QY 325 aagcagatcctggtatggtgaaactcctcacaaagaattgctcattgattc 384
Db 6396 aagcagatcctggtgagcggtctcactcactcactaagcgacatcgacacttgactg 6455
QY 385 aag 387
Db 6456 aag 6458

RESULT 14
ABA09608
ID ABA09608 standard; DNA: 1120 BP.
XX ABA09608;
AC ABA09608;
XX 15-JAN-2002 (first entry)
XX Human bone marrow expressed oligonucleotide SEQ ID NO: 34.
DE Human bone marrow expressed oligonucleotide SEQ ID NO: 34.
XX
XX Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;
KW antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
KW antilicer; fungicide; antidiabetic; antiasthmatic; antiallergic;
KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
KW nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
XX
XX Homo sapiens.
OS
XX WO200174836-A1.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10472.
PE
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
PR 23-AUG-2000; 2000US-0649267.
PR 30-NOV-2000; 2000US-250583P.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
PI
XX WPI: 2001-626375/72.
DR P-PSDB; ABB12364.
XX
XX New bone marrow-expressed nucleic acids and polypeptides, useful for
PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
PT and increasing hematopoiesis, stem cell survival and bone growth and
PT remodeling
XX
XX Claim 1; Page 182; 380pp; English.
PS
XX The present invention relates to bone marrow expressed polynucleotides
CC and proteins. These sequences can be used in the treatment of
CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
CC and peripheral nervous system diseases and neuropathies, such as
CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
CC cell disorders, platelet disorders, stem cell disorders, bone
CC degenerative disorders, autoimmune disorders, for example multiple
CC sclerosis, diabetes and arthritis, viral and bacterial infections,
CC allergies and blood coagulation disorders. The present sequence is a DNA
CC of the invention.
XX
XX Sequence 1120 BP; 271 A; 304 C; 315 G; 230 T; 0 other;

Query Match 29.0%; Score 228.8; DB 22; Length 1120;
Best Local Similarity 96.8%; Pred. No. 3e-55;
Matches 244; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 539 agcccttggtcttggaagctgacatgtgtgacataaggcgtcatcattactccttaa 598
Db 23 agcccttggtcttggaagctgacatgtgtgacataaggcgtcatcattactccttaa 82
QY 599 gtgagacatccctctctcttggaagacagcaggaacactggaataatcacacag 658
Db 83 gtgagacatccctctctcttggaagacagcaggaacactggaataatcacacag 142
QY 659 tgaattacgacttgatgaaatctctcagc-catacgagcagctggtccaaagacttt 717
Db 143 tgaattacgacttgatgaaatctctcagcagcagcagcagcagcagcagcagcagc 202
QY 718 attcggaaagcttctggttaagaaagaccggaaagcgtcacaatccaaggccttga 777
Db 203 attcggaaagcttctggttaagaaagaccggaaagcgtcacaatccaaggccttga 262
QY 778 caccctcgatc 789
Db 263 caccctcgatc 274

RESULT 15
ABA09692
ID ABA09692 standard; DNA: 1505 BP.
XX ABA09692;
AC ABA09692;
XX
XX 15-JAN-2002 (first entry)
XX
XX Human bone marrow expressed oligonucleotide SEQ ID NO: 201.
DE
XX
XX Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;
KW antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
KW antilicer; fungicide; antidiabetic; antiasthmatic; antiallergic;
KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
KW nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
XX
XX Homo sapiens.
OS
XX WO200174836-A1.
PN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US10472.
PE
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
PR 23-AUG-2000; 2000US-0649267.
PR 30-NOV-2000; 2000US-250583P.
XX
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
PI
XX WPI: 2001-626375/72.
DR
XX New bone marrow-expressed nucleic acids and polypeptides, useful for
PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
PT and increasing hematopoiesis, stem cell survival and bone growth and
PT remodeling
XX
XX Claim 1; Page 276-277; 380pp; English.
PS
XX The present invention relates to bone marrow expressed polynucleotides
CC and proteins. These sequences can be used in the treatment of
CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
CC and peripheral nervous system diseases and neuropathies, such as
CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
CC cell disorders, platelet disorders, stem cell disorders, bone
CC degenerative disorders, autoimmune disorders, for example multiple

CC sclerostis, diabetes and arthritis; viral and bacterial infections,
CC allergies and blood coagulation disorders. The present sequence is a DNA
CC of the invention.

XX
SQ Sequence 1505 BP; 417 A; 355 C; 399 G; 334 T; 0 other;

Query Match 29.0%; Score 228.8; DB 22; Length 1505;
Best Local Similarity 96.8%; Pred. No. 3.5e-55;
Matches 244; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

```
QY 539 agccctggcttgagagctgacatgtgagatagaggctacacactacatccctcttaa 598
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 23 agccctgagctcggagctcgacacgtgagcatagagcgtcacctacatccctcttaa 82
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 599 gtgagacatcccttctctctgagagacagaaacagaaactgtgcaaatatcacatcag 658
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 83 gtgagacatcccttctctctgagagacagaaacagaaactgtgcaaatatcacatcag 142
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 659 tgaagtaacgacttgaatgaggaatctctcagc-catacgaagcagctgccaaggacttt 717
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 143 tgaagtaacgacttgaatgaggaatctctcagcagcagcagcagcagcagcagcagcag 202
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 718 attcgaagcttctgttaagaagaccggaacggtcacatccaaagaggtcttcaga 777
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 203 attcgaagcttctgtgttaagaagaccggaacggtcacatccaaagaggtcttcaga 262
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 778 cacccttgatc 789
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 263 cacccttgatc 274
```

Search completed: May 18, 2002, 02:18:08
Job time: 15072 sec